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Sequence Listing was accepted.

See attached Validation Report.

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Reviewer: Anne Corrigan

Timestamp: [year=2007; month=12; day=3; hr=15; min=2; sec=55; ms=353; ]

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Application No: 10563551

Version No: 1.0

Input Set:

Output Set:

Started: 2007-12-03 11:21:33.515

Finished: 2007-12-03 11:21:38.422

Elapsed: 0 hr(s) 0 min(s) 4 sec(s) 907 ms

Total Warnings: 9

Total Errors: 4

No. of SeqIDs Defined: 11

Actual SeqID Count: 11

Error code	Error Description
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W 213	Artificial or Unknown found in <213> in SEQ ID (2)
W 213	Artificial or Unknown found in <213> in SEQ ID (3)
W 213	Artificial or Unknown found in <213> in SEQ ID (4)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (5)
W 213	Artificial or Unknown found in <213> in SEQ ID (7)
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W 213	Artificial or Unknown found in <213> in SEQ ID (11)
E 257	Invalid sequence data feature in <221> in SEQ ID (11)
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# SEQUENCE LISTING

<110> Ding, Jeak Ling  
 Ho, Bow  
 National University of Singapore

<120> Sushi Peptide Multimer

<130> 040184-000400US

<140> 10563551

<141> 2007-12-03

<150> CA 2,432,972

<151> 2003-07-04

<150> WO PCT/SG04/00194

<151> 2004-07-02

<160> 11

<170> PatentIn Ver. 2.1

<210> 1

<211> 34

<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence:synthetic  
 34-mer Sushi-3 peptide (S3 peptide), residues  
 268-301 of Factor C, Sushi3 domain, LPS-binding  
 motif

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Leu Met

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 34-mer Sushi-3delta peptide (S3delta peptide)

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Leu Met

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motif S3 PCR amplification forward primer

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Val Leu Gly Leu Leu Ala Gln Lys Met Arg Pro Val Gln Ser Lys Gly  
15 20 25

gta gat cta ggc ttg tgt gat gaa acg agg ttc gag tgt aag tgt ggc 146  
Val Asp Leu Gly Leu Cys Asp Glu Thr Arg Phe Glu Cys Lys Cys Gly

30	35	40	
gat cca ggc tat gtg ttc aac att cca gtg aaa caa tgt aca tac ttt			194
Asp Pro Gly Tyr Val Phe Asn Ile Pro Val Lys Gln Cys Thr Tyr Phe			
45	50	55	
tat cga tgg agg ccg tat tgt aaa cca tgt gat gac ctg gag gct aag			242
Tyr Arg Trp Arg Pro Tyr Cys Lys Pro Cys Asp Asp Leu Glu Ala Lys			
60	65	70	75
gat att tgt cca aag tac aaa cga tgt caa gag tgt aag gct ggt ctt			290
Asp Ile Cys Pro Lys Tyr Lys Arg Cys Gln Glu Cys Lys Ala Gly Leu			
80	85	90	
gat agt tgt gtt act tgt cca cct aac aaa tat ggt act tgg tgt agc			338
Asp Ser Cys Val Thr Cys Pro Pro Asn Lys Tyr Gly Thr Trp Cys Ser			
95	100	105	
ggg gaa tgt cag tgt aag aat gga ggt atc tgt gac cag agg aca gga			386
Gly Glu Cys Gln Cys Lys Asn Gly Gly Ile Cys Asp Gln Arg Thr Gly			
110	115	120	
gct tgt gca tgt cgt gac aga tat gaa ggg gtg cac tgt gaa att ctc			434
Ala Cys Ala Cys Arg Asp Arg Tyr Glu Gly Val His Cys Glu Ile Leu			
125	130	135	
aaa ggt tgt cct ctt ctt cca tcg gat tct cag gtt cag gaa gtc aga			482
Lys Gly Cys Pro Leu Leu Pro Ser Asp Ser Gln Val Gln Glu Val Arg			
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Asn Pro Pro Asp Asn Pro Gln Thr Ile Asp Tyr Ser Cys Ser Pro Gly			
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Phe Lys Leu Lys Gly Met Ala Arg Ile Ser Cys Leu Pro Asn Gly Gln			
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Trp Ser Asn Phe Pro Pro Lys Cys Ile Arg Glu Cys Ala Met Val Ser			
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Ser Pro Glu His Gly Lys Val Asn Ala Leu Ser Gly Asp Met Ile Glu			
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Gly Ala Thr Leu Arg Phe Ser Cys Asp Ser Pro Tyr Tyr Leu Ile Gly			
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caa gaa aca tta acc tgt cag ggt aat ggt cag tgg aat gga cag ata			770
Gln Glu Thr Leu Thr Cys Gln Gly Asn Gly Gln Trp Asn Gly Gln Ile			
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cca caa tgt aag aac ttg gtc ttc tgt cct gac ctg gat cct gta aac			818
Pro Gln Cys Lys Asn Leu Val Phe Cys Pro Asp Leu Asp Pro Val Asn			
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His Ala Glu His Lys Val Lys Ile Gly Val Glu Gln Lys Tyr Gly Gln	
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Phe Pro Gln Gly Thr Glu Val Thr Tyr Thr Cys Ser Gly Asn Tyr Phe	
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Leu Met Gly Phe Asp Thr Leu Lys Cys Asn Pro Asp Gly Ser Trp Ser	
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Gly Ser Gln Pro Ser Cys Val Lys Val Ala Asp Arg Glu Val Asp Cys	
320 325 330	
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Asp Ser Lys Ala Val Asp Phe Leu Asp Asp Val Gly Glu Pro Val Arg	
335 340 345	
atc cac tgt cct gct ggc tgt tct ttg aca gct ggt act gtg tgg ggt	1106
Ile His Cys Pro Ala Gly Cys Ser Leu Thr Ala Gly Thr Val Trp Gly	
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aca gcc ata tac cat gaa ctt tcc tca gtg tgt cgt gca gcc atc cat	1154
Thr Ala Ile Tyr His Glu Leu Ser Ser Val Cys Arg Ala Ala Ile His	
365 370 375	
gct ggc aag ctt cca aac tct gga gga gcg gtg cat gtt gtg aac aat	1202
Ala Gly Lys Leu Pro Asn Ser Gly Gly Ala Val His Val Val Asn Asn	
380 385 390 395	
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400 405 410	
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Glu Glu Leu Lys Ser Leu Ala Arg Ser Phe Arg Phe Asp Tyr Val Arg	
415 420 425	
tcc tcc aca gca ggt aaa tca gga tgt cct gat gga tgg ttt gag gta	1346
Ser Ser Thr Ala Gly Lys Ser Gly Cys Pro Asp Gly Trp Phe Glu Val	
430 435 440	
gac gag aac tgt gtg tac gtt aca tca aaa cag aga gcc tgg gaa aga	1394
Asp Glu Asn Cys Val Tyr Val Thr Ser Lys Gln Arg Ala Trp Glu Arg	
445 450 455	
gct caa ggt gtg tgt acc aat atg gct gct cgt ctt gct gtg ctg gac	1442
Ala Gln Gly Val Cys Thr Asn Met Ala Ala Arg Leu Ala Val Leu Asp	
460 465 470 475	
aaa gat gta att cca aat tcg ttg act gag act cta cga ggg aaa ggg	1490
Lys Asp Val Ile Pro Asn Ser Leu Thr Glu Thr Leu Arg Gly Lys Gly	
480 485 490	

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Leu Thr Thr Thr Trp Ile Gly Leu His Arg Leu Asp Ala Glu Lys Pro	
495 500 505	
ttt att tgg gag tta atg gat cgt agt aat gtg gtt ctg aat gat aac	1586
Phe Ile Trp Glu Leu Met Asp Arg Ser Asn Val Val Leu Asn Asp Asn	
510 515 520	
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525 530 535	
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Tyr Met Asp Ile Gln Asp Gln Leu Gln Ser Val Trp Lys Thr Lys Ser	
540 545 550 555	
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Cys Phe Gln Pro Ser Ser Phe Ala Cys Met Met Asp Leu Ser Asp Arg	
560 565 570	
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Asn Lys Ala Lys Cys Asp Asp Pro Gly Ser Leu Glu Asn Gly His Ala	
575 580 585	
aca ctt cat gga caa agt att gat ggg ttc tat gct ggt tct tct ata	1826
Thr Leu His Gly Gln Ser Ile Asp Gly Phe Tyr Ala Gly Ser Ser Ile	
590 595 600	
agg tac agc tgt gag gtt ctc cac tac ctc agt gga act gaa acc gta	1874
Arg Tyr Ser Cys Glu Val Leu His Tyr Leu Ser Gly Thr Glu Thr Val	
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act tgt aca aca aat ggc aca tgg agt gct cct aaa cct cga tgt atc	1922
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620 625 630 635	
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Lys Val Ile Thr Cys Gln Asn Pro Pro Val Pro Ser Tyr Gly Ser Val	
640 645 650	
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Glu Ile Lys Pro Pro Ser Arg Thr Asn Ser Ile Ser Arg Val Gly Ser	
655 660 665	
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670 675 680	
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Lys Pro Pro Pro Lys Pro Arg Ser Ser Gln Pro Ser Thr Val Asp Leu	
685 690 695	
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gcc atc tac acg tgc gag tcg aga tac tac gaa cta ctt gga tct caa	2210

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Gly Arg Arg Cys Asp Ser Asn Gly Asn Trp Ser Gly Arg Pro Ala Ser	
735 740 745	
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Cys Ile Pro Val Cys Gly Arg Ser Asp Ser Pro Arg Ser Pro Phe Ile	
750 755 760	
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765 770 775	
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acc tac tct gct act gct gag att att gac ccc aat cag ttt aaa atg	2498
Thr Tyr Ser Ala Thr Ala Glu Ile Ile Asp Pro Asn Gln Phe Lys Met	
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tat ctg ggc aag tac tac cgt gat gac agt aga gac gat gac tat gta	2546
Tyr Leu Gly Lys Tyr Tyr Arg Asp Asp Ser Arg Asp Asp Asp Tyr Val	
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Gln Val Arg Glu Ala Leu Glu Ile His Val Asn Pro Asn Tyr Asp Pro	
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ggc aat ctc aac ttt gac ata gcc cta att caa ctg aaa act cct gtt	2642
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860 865 870 875	
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925 930 935	
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Asp Leu Pro Leu Thr Val Thr Glu Asn Met Phe Cys Ala Gly Tyr Lys	



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<212> PRT

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Tyr Lys Arg Cys Gln Glu Cys Lys Ala Gly Leu Asp Ser Cys Val Thr			
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Cys Pro Pro Asn Lys Tyr Gly Thr Trp Cys Ser Gly Glu Cys Gln Cys			

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